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Felicia Walker
(Print Name)

Date: July 27, 2000

Felicia Walker
(Signature)

PATENT APPLICATION **Docket No: 8636**

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application

Batch No. 435-188.000
Notice of Allowance Date: 10/6/99

Inventor's Name(s): Gelfand et al.

Art Unit: 1651

Serial No. 07/873,897, filed April 24, 1992

Examiner: D. Naff

For: **PURIFIED THERMOSTABLE ENZYME**

TRANSMITTAL OF FORMAL DRAWINGS

Assistant Commissioner for Patents
Washington, D.C. 20231

Alameda, CA
July 27, 2000

Draftsperson:

The Notice of Draftsperson's Patent Drawing Review attached to Paper 49, mailed July 17, 2000, indicated that Fig. 1-1 to Fig. 1-6 should be labeled Fig. 1A – 1F. Enclosed are the amended formal drawings, Figures 1-A through 1-F, (six sheets) for filing in the above-identified U.S. Patent Application. The amendments are of a purely formal nature and do not introduce new matter. Applicants request entry of the drawings.

Respectfully submitted,

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10.06.99

TAQ DNA POLYMERASE SEQUENCE

FIG.1-A

```
-120                -100                 -80
      BglII                            PvuII
AAGCTCAGATCTACCTGCCTGAGGGCGTCCGGTTCCAGCTGGCCCTTCCCGAGGGGGAGA

-60                  -40                 -20
GGGAGGCGTTTCTAAAAGCCCTTCAGGACGCTACCCGGGGGCGGGTGGTGGAAGGGTAAC

1                    20                  40                  60
ATGAGGGGGATGCTGCCCCTCTTTGAGCCCAAGGGCCGGGTCCTCCTGGTGGACGGCCAC
MetArgGlyMetLeuProLeuPheGluProLysGlyArgValLeuLeuValAspGlyHis
  1

                     80                 100                 120
CACCTGGCCTACCGCACCTTCCACGCCCTGAAGGGCCTCACCACCAGCCGGGGGGAGCCG
HisLeuAlaTyrArgThrPheHisAlaLeuLysGlyLeuThrThrSerArgGlyGluPro

                    140                 160                 180
GTGCAGGCGGTCTACGGCTTCGCCAAGAGCCTCCTCAAGGCCCTCAAGGAGGACGGGGAC
ValGlnAlaValTyrGlyPheAlaLysSerLeuLeuLysAlaLeuLysGluAspGlyAsp
 41

                    200                 220                 240
GCGGTGATCGTGGTCTTTGACGCCAAGGCCCCCTCCTTCCGCCACGAGGCCTACGGGGGG
AlaValIleValValPheAspAlaLysAlaProSerPheArgHisGluAlaTyrGlyGly

                    260                 280                 300
TACAAGGCGGGCCGGGCCCCCACGCCGGAGGACTTTCCCCGGCAACTCGCCCTCATCAAG
TyrLysAlaGlyArgAlaProThrProGluAspPheProArgGlnLeuAlaLeuIleLys
 81

                    320                 340                 360
                                   XhoI
GAGCTGGTGGACCTCCTGGGGCTGGCGCGCCTCGAGGTCCCGGGCTACGAGGCGGACGAC
GluLeuValAspLeuLeuGlyLeuAlaArgLeuGluValProGlyTyrGluAlaAspAsp
```

TAQ DNA POLYMERASE SEQUENCE

FIG.1-B

380 400 420

GTCCTGGCCAGCCTGGCCAAGAAGGCGGAAAAGGAGGGCTACGAGGTCCGCATCCTCACC
ValLeuAlaSerLeuAlaLysLysAlaGluLysGluGlyTyrGluValArgIleLeuThr
121

440 460 480

GCCGACAAAGACCTTTACCAGCTCCTTTCCGACCGCATCCACGTCCTCCACCCCGAGGG
AlaAspLysAspLeuTyrGlnLeuLeuSerAspArgIleHisValLeuHisProGluGly

500 520 540

Asp718

***TACC*TCATCACCCCGGCCTGGCTTTGGAAAAGTACGGCCTGAGGCCCGACCAGTGGGCC**
TyrLeuIleThrProAlaTrpLeuTrpGluLysTyrGlyLeuArgProAspGlnTrpAla
161

560 580 600

GACTACCGGGCCCTGACCGGGGACGAGTCCGACAACCTTCCCGGGGTCAAGGGCATCGGG
AspTyrArgAlaLeuThrGlyAspGluSerAspAsnLeuProGlyValLysGlyIleGly

620 640 660

HindIII

GAGAAGACGGCGAGG*AAGCTT*CTGGAGGAGTGGGGGAGCCTGGAAGCCCTCCTCAAGAAC
GluLysThrAlaArgLysLeuLeuGluGluTrpGlySerLeuGluAlaLeuLeuLysAsn
201

680 700 720

CTGGACCGGCTGAAGCCCGCCATCCGGGAGAAGATCCTGGCCCACATGGACGATCTGAAG
LeuAspArgLeuLysProAlaIleArgGluLysIleLeuAlaHisMetAspAspLeuLys

740 760 780

CTCTCCTGGGACCTGGCCAAGGTGCGCACCGACCTGCCCCTGGAGGTGGACTTCGCCAAA
LeuSerTrpAspLeuAlaLysValArgThrAspLeuProLeuGluValAspPheAlaLys
241

800 820 840

AGGCGGGAGCCCGACCGGGAGAGGCTTAGGGCCTTTCTGGAGAGGCTTGAGTTTGGCAGC
ArgArgGluProAspArgGluArgLeuArgAlaPheLeuGluArgLeuGluPheGlySer

TAQ DNA POLYMERASE SEQUENCE

FIG.1-C

```
                 860                 880                 900
                                  BstXI
          .         .         .         .         .         .
**CTCCTCCACGAGTTCGGCCTTCTGGAAAGCCCCAAGGCCCTGGAGGAGGCCCCCTGGCCC
LeuLeuHisGluPheGlyLeuLeuGluSerProLysAlaLeuGluGluAlaProTrpPro
281                           290

                 920                 940                 960
          .         .         .         .         .         .
CCGCCGGAAGGGGCCTTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGAT
ProProGluGlyAlaPheValGlyPheValLeuSerArgLysGluProMetTrpAlaAsp

                 980                1000                1020
          .         .         .         .         .         .
CTTCTGGCCCTGGCCGCCGCCAGGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTATAAA
LeuLeuAlaLeuAlaAlaAlaArgGlyGlyArgValHisArgAlaProGluProTyrLys
321

                1040                1060                1080
          .         .         .         .         .         .
GCCCTCAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGCC
AlaLeuArgAspLeuLysGluAlaArgGlyLeuLeuAlaLysAspLeuSerValLeuAla

                1100                1120                1140
          .         .         .         .         .         .
CTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCCCATGCTCCTCGCCTACCTCCTG
LeuArgGluGlyLeuGlyLeuProProGlyAspAspProMetLeuLeuAlaTyrLeuLeu
361

                1160                1180                1200
          .         .         .         .         .         .
GACCCTTCCAACACCACCCCCGAGGGGGTGGCCCGGCGCTACGGCGGGGAGTGGACGGAG
AspProSerAsnThrThrProGluGlyValAlaArgArgTyrGlyGlyGluTrpThrGlu

                1220                1240                1260
          .         .         .         .         .         .
GAGGCGGGGGAGCGGGCCGCCCTTTCCGAGAGGCTCTTCGCCAACCTGTGGGGGAGGCTT
GluAlaGlyGluArgAlaAlaLeuSerGluArgLeuPheAlaAsnLeuTrpGlyArgLeu
401

                1280                1300                1320
          .         .         .         .         .         .
GAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAGGTGGAGAGGCCCCTTTCCGCTGTC
GluGlyGluGluArgLeuLeuTrpLeuTyrArgGluValGluArgProLeuSerAlaVal
```

TAQ DNA POLYMERASE SEQUENCE

FIG.1-D

1340 1360 1380

CTGGCCCACATGGAGGCCACGGGGGTGCGCCTGGACGTGGCCTATCTCAGGGCCTTGTCC
LeuAlaHisMetGluAlaThrGlyValArgLeuAspValAlaTyrLeuArgAlaLeuSer
441

1400 1420 1440
XhoI

CTGGAGGTGGCCGAGGAGATCGCCCGC*CTCGAG*GCCGAGGTCTTCCGCCTGGCCGGCCAC
LeuGluValAlaGluGluIleAlaArgLeuGluAlaGluValPheArgLeuAlaGlyHis

1460 1480 1500
PvuII

CCCTTCAACCTCAACTCCCGGGAC*CAGCTG*GAAAGGGTCCTCTTTGACGAGCTAGGGCTT
ProPheAsnLeuAsnSerArgAspGlnLeuGluArgValLeuPheAspGluLeuGlyLeu
481

1520 1540 1560

CCCGCCATCGGCAAGACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCCGTCCTGGAG
ProAlaIleGlyLysThrGluLysThrGlyLysArgSerThrSerAlaAlaValLeuGlu

1580 1600 1620
PstI *SacI*

GCCCTCCGCGAGGCCCACCCCATCGTGGAGAAGATC*CTGCAG*TACCGG*GAGCTC*ACCAAG
AlaLeuArgGluAlaHisProIleValGluLysIleLeuGlnTyrArgGluLeuThrLys
521

1640 1660 1680

CTGAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCCAGGACGGGCCGCCTC
LeuLysSerThrTyrIleAspProLeuProAspLeuIleHisProArgThrGlyArgLeu

1700 1720 1740

CACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTCCGATCCCAAC
HisThrArgPheAsnGlnThrAlaThrAlaThrGlyArgLeuSerSerSerAspProAsn
561

1760 1780 1800
BamHI

CTCCAGAACATCCCCGTCCGCACCCCGCTTGGGCAGA*GGATCC*GCCGGGCCTTCATCGCC
LeuGlnAsnIleProValArgThrProLeuGlyGlnArgIleArgArgAlaPheIleAla

TAQ DNA POLYMERASE SEQUENCE

FIG.1-E

1820 1840 1860

SacI

GAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAGATA*GAGCTC*AGGGTGCTGGCC

GluGluGlyTrpLeuLeuValAlaLeuAspTyrSerGlnIleGluLeuArgValLeuAla

601

1880 1900 1920

CACCTCTCCGGCGACGAGAACCTGATCCGGGTCTTCCAGGAGGGGCGGGACATCCACACG

HisLeuSerGlyAspGluAsnLeuIleArgValPheGlnGluGlyArgAspIleHisThr

1940 1960 1980

PvuII

GAGACCGC*CAGCTG*GATGTTCGGCGTCCCCCGGGAGGCCGTGGACCCCCTGATGCGCCGG

GluThrAlaSerTrpMetPheGlyValProArgGluAlaValAspProLeuMetArgArg

641

2000 2020 2040

GCGGCCAAGACCATCAACTTCGGGGTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAG

AlaAlaLysThrIleAsnPheGlyValLeuTyrGlyMetSerAlaHisArgLeuSerGln

2060 2080 2100

NheI

GA*GCTAGC*CATCCCTTACGAGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTC

GluLeuAlaIleProTyrGluGluAlaGlnAlaPheIleGluArgTyrPheGlnSerPhe

681

2120 2140 2160

CCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTG

ProLysValArgAlaTrpIleGluLysThrLeuGluGluGlyArgArgArgGlyTyrVal

2180 2200 2220

GAGACCCTCTTCGGCCGCCGCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGTG

GluThrLeuPheGlyArgArgArgTyrValProAspLeuGluAlaArgValLysSerVal

721

TAQ DNA POLYMERASE SEQUENCE

```
                      2240                 2260                 2280
          .          .          .          .          .          .
CGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGCCGACCTC
ArgGluAlaAlaGluArgMetAlaPheAsnMetProValGlnGlyThrAlaAlaAspLeu
741

                      2300                 2320                 2340
          .          .          .          .          .          .
ATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGGGGCCAGGATGCTC
MetLysLeuAlaMetValLysLeuPheProArgLeuGluGluMetGlyAlaArgMetLeu

                      2360                 2380                 2400
                                 XhoI
          .          .          .          .          .          .
CTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCCAAAAGAGAGGGCGGAGGCCGTGGCC
LeuGlnValHisAspGluLeuValLeuGluAlaProLysGluArgAlaGluAlaValAla
781

                      2420                 2440                 2460
          .          .          .          .          .          .
CGGCTGGCCAAGGAGGTCATGGAGGGGGTGTATCCCCTGGCCGTGCCCCTGGAGGTGGAG
ArgLeuAlaLysGluValMetGluGlyValTyrProLeuAlaValProLeuGluValGlu

                      2480                 2500
          .          .          .          .
GTGGGGATAGGGGAGGACTGGCTCTCCGCCAAGGAGTGATACCACC
ValGlyIleGlyGluAspTrpLeuSerAlaLysGluEnd
821                                 832
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FIG. 1-F